Applications of Hi-C technology in epigenetics and genome assembly

Abstract

Hi-C is a method for mapping the three-dimensional (3D) structure of chromosomes within the nucleus of a cell. The Hi-C method works by crosslinking and ligating genomic DNA fragments in situ, followed by high-throughput sequencing to determine the proximity of genomic loci. This information is used to build a map of chromosome interactions, which provides insights into the functional relationships between genomic elements and their roles in gene regulation, genome stability, and cellular processes. In addition, it has widely used to scaffold draft genomes to chromosomal scale which provide the contiguity to the draft genomes. The advent of Hi-C opened the door for researchers to study the 3D organization of the genome and its role in fundamental biological processes as well as produce high quality reference genomes.

In this seminar, we will discuss the applications of Hi-C technology. We will also share two case studies that using Dovetail Hi-C technology. The first case study involved the study of the potential of targeting SWI/SNF ATPases as a therapeutic strategy for treating prostate cancer that is dependent on enhancer activity. The study provides insights into the understanding of the molecular mechanisms involved and the challenges associated with developing effective therapies targeting the SWI/SNF complex in prostate cancer.

The second case study will be focusing on the role of epigenetic changes in the aging process. The study provides an overview of the epigenetic modifications that occur in DNA, such as DNA methylation and histone modifications, and how these modifications can affect gene expression and cellular function. The study highlights the importance of understanding these epigenetic changes in the aging process and the potential for epigenetic interventions as a therapeutic approach for age-related diseases.

Lastly, we will discuss the utility of Hi-C technology in chromosomal scale genome assembly, haplotype resolved assembly and polyploidy genome assembly.

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